

BLASTN 2.2.6 [Apr-09-2003]

1-434

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1070314417-22036-142275428472.BLASTQ3

Query=

(896 letters)

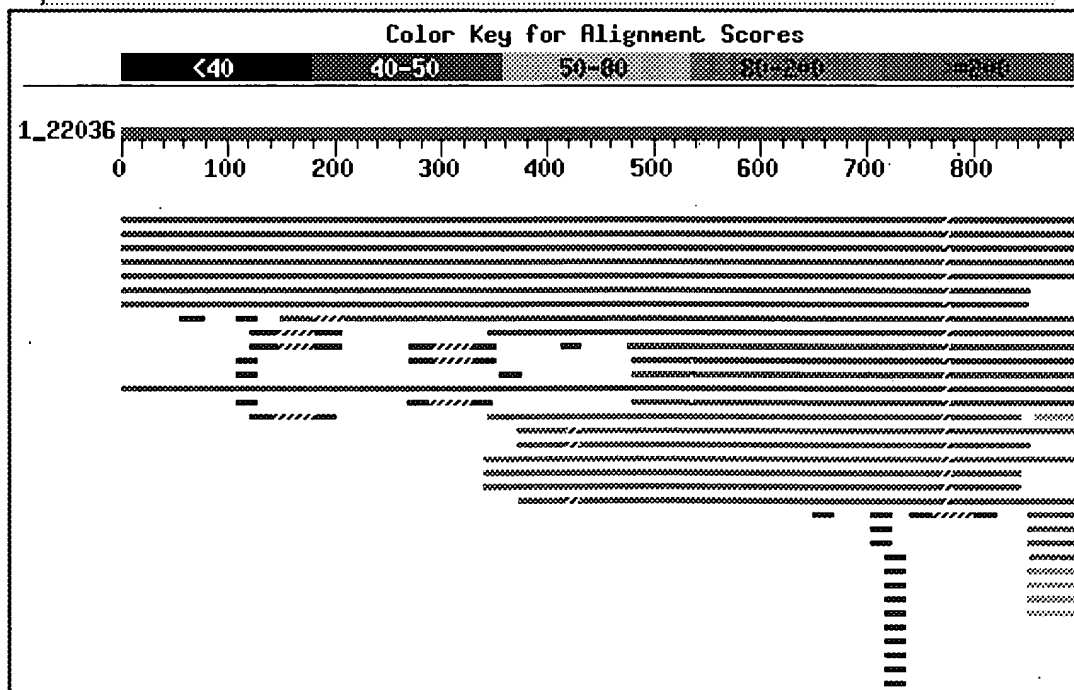
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

1,981,639 sequences; 9,522,297,199 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)Distribution of 173 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

	Score (bits)	E Value
--	-----------------	------------

gi 33329251 gb AF531258.1	Homo sapiens K-Cl cotransporter ...	240	4e-60	
gi 30704980 gb BC051709.1	Homo sapiens mRNA similar to sol...	240	4e-60	
gi 22416401 gb AF314931.1 F314931S01	Homo sapiens potassium...	240	4e-60	
gi 22657552 gb AC025678.7	Homo sapiens chromosome 15, clon...	240	4e-60	
gi 28201588 gb AC021822.21	Homo sapiens chromosome 15, clo...	240	4e-60	
gi 34367354 emb BX648195.1 HSM808343	Homo sapiens mRNA; cDN...	240	4e-60	
gi 5106522 gb AF105366.1 AF105366	Homo sapiens K-Cl cotrans...	240	4e-60	
gi 21707904 gb BC033894.1	Homo sapiens, solute carrier fam...	238	1e-59	
gi 6693797 gb AF116242.1 AF116242	Homo sapiens K-Cl cotrans...	238	1e-59	
gi 33329255 gb AF531260.1	Homo sapiens K-Cl cotransporter ...	236	6e-59	
gi 33329253 gb AF531259.1	Homo sapiens K-Cl cotransporter ...	234	2e-58	
gi 30704365 gb BC051744.1	Homo sapiens cDNA clone IMAGE:48...	234	2e-58	
gi 19110890 gb AF477977.1	Homo sapiens K-Cl cotransporter ...	232	9e-58	
gi 15208176 dbj AB070168.1	Macaca fascicularis testis cDNA...	232	9e-58	
gi 34857569 ref XM_345416.1	Rattus norvegicus similar to K...	192	8e-46	
gi 38073247 gb AY429045.1	Rattus norvegicus brain-specific...	174	2e-40	
gi 38073245 gb AY429044.1	Rattus norvegicus K-Cl cotranspo...	174	2e-40	
gi 38565927 gb BC062099.1	Mus musculus cDNA clone MGC:6965...	168	1e-38	
gi 15042076 gb AF211854.1 AF211854	Mus musculus K-Cl cotran...	168	1e-38	
gi 21261919 emb AL713853.6	Mouse DNA sequence from clone R...	168	1e-38	
gi 37575102 gb AY387484.1	Rattus norvegicus furosemide-sen...	167	4e-38	
gi 4826779 ref NM_005135.1	Homo sapiens solute carrier fam...	92	2e-15	
gi 22416403 gb AF314933.1 F314931S03	Homo sapiens potassium...	92	2e-15	
gi 4585228 gb AF108831.1 AF108831	Homo sapiens K:Cl cotrans...	92	2e-15	
gi 34535353 dbj AK128133.1	Homo sapiens cDNA FLJ46254 fis,...	90	8e-15	
gi 19526768 ref NM_133648.1	Mus musculus solute carrier fa...	68	3e-08	
gi 12861186 dbj AK020568.1	Mus musculus adult male urinary...	68	3e-08	
gi 15042078 gb AF211855.1 AF211855	Mus musculus K-Cl cotran...	68	3e-08	
gi 23894529 emb AL683897.5	Mouse DNA sequence from clone R...	68	3e-08	
gi 38073243 gb AY429043.1	Rattus norvegicus K-Cl cotranspo...	60	7e-06	
gi 33636819 gb AC102255.10	Mus musculus chromosome 18, clo...	42	1.7	
gi 29895263 gb AE017003.1	Bacillus cereus ATCC 14579 secti...	42	1.7	
gi 30255837 gb AE017029.1	Bacillus anthracis str. Ames sec...	42	1.7	
gi 22947051 gb AE003782.3	Drosophila melanogaster chromoso...	42	1.7	
gi 5430741 gb AC006415.11 AC006415	Drosophila melanogaster,...	42	1.7	
gi 38371866 gb AC079443.48	Mus musculus clone rp23-381f7 m...	40	6.8	
gi 23462947 gb AC121996.3	Mus musculus BAC clone RP24-312F...	40	6.8	
gi 34787443 gb AC006945.17	Mus musculus clone ct7-453113 m...	40	6.8	
gi 29541262 gb AE016962.1	Coxiella burnetii strain RSA 493...	40	6.8	
gi 21450414 gb AC009368.8	Drosophila melanogaster 3L BAC R...	40	6.8	
gi 21306592 gb AC010003.8	Drosophila melanogaster 3L BAC R...	40	6.8	
gi 20258593 gb AC107061.6	Homo sapiens BAC clone RP11-749L...	40	6.8	
gi 23093196 gb AE003521.3	Drosophila melanogaster chromoso...	40	6.8	
gi 26665708 gb AC134229.2	Oryza sativa (japonica cultivar-...	40	6.8	
gi 26081972 dbj AK030754.1	Mus musculus 8 days embryo whol...	40	6.8	
gi 14285260 emb AJ306650.1 CPO306650	Cavia porcellus mRNA f...	40	6.8	
gi 13259350 gb AF313891.1 AF313891	Uncultured methanogen MR...	40	6.8	
gi 13259348 gb AF313890.1 AF313890	Uncultured methanogen MR...	40	6.8	
gi 13259346 gb AF313889.1 AF313889	Uncultured methanogen MR...	40	6.8	
gi 13259344 gb AF313888.1 AF313888	Uncultured methanogen MR...	40	6.8	
gi 13259342 gb AF313887.1 AF313887	Uncultured methanogen MR...	40	6.8	

<u>gi 13259340 gb AF313886.1 AF313886</u>	Uncultured methanogen MR...	<u>40</u>	6.8
<u>gi 13259338 gb AF313885.1 AF313885</u>	Uncultured methanogen MR...	<u>40</u>	6.8
<u>gi 13259336 gb AF313884.1 AF313884</u>	Uncultured methanogen MR...	<u>40</u>	6.8
<u>gi 13259334 gb AF313883.1 AF313883</u>	Uncultured methanogen MR...	<u>40</u>	6.8
<u>gi 13259332 gb AF313882.1 AF313882</u>	Uncultured methanogen MR...	<u>40</u>	6.8
<u>gi 11863362 emb AL138960.16 </u>	Human DNA sequence from clone ...	<u>40</u>	6.8
<u>gi 21655368 emb AL671897.6 </u>	Mouse DNA sequence from clone R...	<u>40</u>	6.8

Alignments

Get selected sequences

Select all

Deselect all

☒ >gi|33329251|gb|AF531258.1| ☒ Homo sapiens K-C1 cotransporter KCC3a-X2M isoform
complete cds; alternatively spliced
Length = 4215

Score = 240 bits (121), Expect = 4e-60

Identities = 121/121 (100%)

Strand = Plus / Plus

Query: 59 tgagtagaagtattccttagttggggcctttttgtgtggtgtgaatcaagggttattgaaatg 118
|||||
Sbjct: 1 tgagtagaagtattccttagttggggcctttttgtgtggtgtgaatcaagggttattgaaatg 60

Query: 119 tggtatttttcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 178
|||||
Sbjct: 61 tggtatttttcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 120

Query: 179 t 179

|

Sbjct: 121 t 121

Score = 238 bits (120), Expect = 1e-59

Identities = 120/120 (100%)

Strand = Plus / Plus

Query: 537 caggtttgtcagacaccagtcctcgacctcagctctcgatctagttcccagtaagattta 596
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Sbjct: 241 caggtttgtcagacaccagtcctcgacctcagctctcgatctagttcccagtaagattta 300

Query: 597 gctcccggaagcggtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 656
|||||
Sbjct: 301 gctcccggaagcggtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 360

Score = 232 bits (117), Expect = 9e-58

Identities = 119/120 (99%)

Strand = Plus / Plus

Query: 417 ccaccaccaagatggcttcagttcggttcatggtgacaccgacaaagatcgatgacattc 476
|||||
Sbjct: 181 ccaccaccaagatggcttcagttcggttcatggtgacaccgacaaagatcgatgacattc 240

Query: 477 caggtttgtcagacaccagtcgggacntcagctctcgatctagttcccgagtaagattta 536
|||||
Sbjct: 241 caggtttgtcagacaccagtcgggacntcagctctcgatctagttcccgagtaagattta 300

Score = 228 bits (115), Expect = 1e-56
Identities = 115/115 (100%)
Strand = Plus / Plus

Query: 657 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 716
|||||
Sbjct: 301 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 360

Query: 717 ccaccacttcgctggcaactgttgactggatccaccagtgaccggacttctca 771
|||||
Sbjct: 361 ccaccacttcgctggcaactgttgactggatccaccagtgaccggacttctca 415

Score = 196 bits (99), Expect = 5e-47
Identities = 113/120 (94%)
Strand = Plus / Plus

Query: 179 tgttatTTTTcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 238
|||||
Sbjct: 61 tgttatTTTTcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 120

Query: 239 tttgcgaggttccccccacnnnnnnngttcttaaaaagaacaaaatgcatcctccagaaa 298
|||||
Sbjct: 121 tttgcgaggttccccccacttttttgttcttaaaaagaacaaaatgcatcctccagaaa 180

Score = 176 bits (89), Expect = 5e-41
Identities = 112/121 (92%), Gaps = 2/121 (1%)
Strand = Plus / Plus

Query: 299 tttgcgaggttccccccacnnnnnnngttcttaaaaagaacaaaatgcatcctccagaaa 358
|||||
Sbjct: 121 tttgcgaggttccccccacttttttgttcttaaaaagaacaaaatgcatcctccagaaa 180

Query: 359 --accaccaagatggcttcagttcggttcatggtgacaccgacaaagatcgatgacattc 416
|||||
Sbjct: 181 ccaccaccaagatggcttcagttcggttcatggtgacaccgacaaagatcgatgacattc 240

Query: 417 c 417

Sbjct: 241 c 241


Score = 149 bits (75), Expect = 1e-32
Identities = 75/75 (100%)
Strand = Plus / Plus

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|||||
Sbjct: 363 accacttcgctggcaactggtgcactggatccaccagtgaccggacttctcaccgccag 422

Query: 839 gatgtcatcgaggac 853
|||||
Sbjct: 423 gatgtcatcgaggac 437

Score = 119 bits (60), Expect = 9e-24
Identities = 60/60 (100%)
Strand = Plus / Plus

Query: 1 tgagtagaagtattcttagttggggctttttgtgtggtgtgaatcaagggtattgaaatg 60
|||||
Sbjct: 1 tgagtagaagtattcttagttggggctttttgtgtggtgtgaatcaagggtattgaaatg 60

 >gi|30704980|gb|BC051709.1 Homo sapiens mRNA similar to solute carrier family 1
(potassium/chloride transporters), member 6 (cDNA clone
IMAGE:5298663)
Length = 5437

Score = 240 bits (121), Expect = 4e-60
Identities = 121/121 (100%)
Strand = Plus / Plus

Query: 59 tgagtagaagtattcttagttggggctttttgtgtggtgtgaatcaagggtattgaaatg 118
|||||
Sbjct: 1216 tgagtagaagtattcttagttggggctttttgtgtggtgtgaatcaagggtattgaaatg 1275

Query: 119 tgttatTTTTcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 178
|||||
Sbjct: 1276 tgttatTTTTcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 1335

Query: 179 t 179
|
Sbjct: 1336 t 1336

Score = 238 bits (120), Expect = 1e-59

Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 537 caggtttgtcagacaccagtcgacctcagctctcgatctagttcccagtaagattta 596
|||||
Sbjct: 1456 caggtttgtcagacaccagtcgacctcagctctcgatctagttcccagtaagattta 1515

Query: 597 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 656
|||||
Sbjct: 1516 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 1575

Score = 234 bits (118), Expect = 2e-58
Identities = 118/118 (100%)
Strand = Plus / Plus

Query: 779 accacttcgctggcaactgttgactggatccaccagtgaccggacttctcacccccag 838
|||||
Sbjct: 1578 accacttcgctggcaactgttgactggatccaccagtgaccggacttctcacccccag 1637

Query: 839 gatgtcatcgaggacctgagtcagaactccatcacaggggaacacagccaactgtag 896
|||||
Sbjct: 1638 gatgtcatcgaggacctgagtcagaactccatcacaggggaacacagccaactgtag 1695

Score = 232 bits (117), Expect = 9e-58
Identities = 119/120 (99%)
Strand = Plus / Plus

Query: 417 ccaccaccaagatggcttcagttcggttcattggtgacaccgacaaagatcgatgacattc 476
|||||
Sbjct: 1396 ccaccaccaagatggcttcagttcggttcattggtgacaccgacaaagatcgatgacattc 1455

Query: 477 caggtttgtcagacaccagtcgacntcagctctcgatctagttcccagtaagattta 536
|||||
Sbjct: 1456 caggtttgtcagacaccagtcgacntcagctctcgatctagttcccagtaagattta 1515

Score = 228 bits (115), Expect = 1e-56
Identities = 115/115 (100%)
Strand = Plus / Plus

Query: 657 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 716
|||||
Sbjct: 1516 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 1575

Query: 717 ccaccacttcgctggcaactgttgactggatccaccagtgaccggacttctca 771
|||||
Sbjct: 1576 ccaccacttcgctggcaactgttgactggatccaccagtgaccggacttctca 1630

Score = 196 bits (99), Expect = 5e-47
Identities = 113/120 (94%)
Strand = Plus / Plus

Query: 179 tggtatttttcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 238
|||||
Sbjct: 1276 tggtatttttcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 1335

Query: 239 tttgcgaggttccccccacnnnnnnngttcttaaaaagaacaaaatgcatcctccagaaa 298
|||||
Sbjct: 1336 tttgcgaggttccccccacttttttgttcttaaaaagaacaaaatgcatcctccagaaa 1395

Score = 176 bits (89), Expect = 5e-41
Identities = 112/121 (92%), Gaps = 2/121 (1%)
Strand = Plus / Plus

Query: 299 tttgcgaggttccccccacnnnnnnngttcttaaaaagaacaaaatgcatcctccagaaa 358
|||||
Sbjct: 1336 tttgcgaggttccccccacttttttgttcttaaaaagaacaaaatgcatcctccagaaa 1395

Query: 359 --accaccaagatggcttcagttcggttcattggtgacaccgacaaagatcgatgacattc 416
|||||
Sbjct: 1396 ccaccaccaagatggcttcagttcggttcattggtgacaccgacaaagatcgatgacattc 1455

Query: 417 c 417
|
Sbjct: 1456 c 1456

Score = 119 bits (60), Expect = 9e-24
Identities = 60/60 (100%)
Strand = Plus / Plus

Query: 1 tgagtagaagtattcttagttggggctttttgtgtggtgtgaatcaagggtattgaaatg 60
|||||
Sbjct: 1216 tgagtagaagtattcttagttggggctttttgtgtggtgtgaatcaagggtattgaaatg 1275

☐ >gi|22416401|gb|AF314931.1|F314931S01 Homo sapiens potassium-chloride transporte
1a
Length = 489

Score = 240 bits (121), Expect = 4e-60
Identities = 121/121 (100%)
Strand = Plus / Plus

Query: 59 tgagtagaagtattcttagttggggccttttgtgtggtgtgaatcaaggttattgaaatg 118
|||||
Sbjct: 1 tgagtagaagtattcttagttggggccttttgtgtggtgtgaatcaaggttattgaaatg 60

Query: 119 tgttatttttcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 178
|||||
Sbjct: 61 tgttatttttcaagttatcttttgtattgcagtcaaaagtagctagcgtaagaggaagat 120

Query: 179 t 179
|
Sbjct: 121 t 121

Score = 238 bits (120), Expect = 1e-59
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 537 caggtttgtcagacaccagtcgacacctcagctctcgatctagttcccagtaagattta 596
|||||
Sbjct: 241 caggtttgtcagacaccagtcgacacctcagctctcgatctagttcccagtaagattta 300

Query: 597 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 656
|||||
Sbjct: 301 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 360

Score = 232 bits (117), Expect = 9e-58
Identities = 119/120 (99%)
Strand = Plus / Plus

Query: 417 ccaccaccaagatggcttcagttcggttcatggtgacaccgacaaagatcgatgacattc 476
|||||
Sbjct: 181 ccaccaccaagatggcttcagttcggttcatggtgacaccgacaaagatcgatgacattc 240

Query: 477 caggtttgtcagacaccagtcgacacntcagctctcgatctagttcccagtaagattta 536
|||||
Sbjct: 241 caggtttgtcagacaccagtcgacacntcagctctcgatctagttcccagtaagattta 300

Score = 228 bits (115), Expect = 1e-56
Identities = 115/115 (100%)
Strand = Plus / Plus

Query: 657 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 716
|||||
Sbjct: 301 gctcccgggaaagcgtgcctgaaacaagccggagtgagcctatgagtgagatgtctgggg 360

Query: 717 ccaccacttcgctggcaactggttgactggatccaccagtgaccggacttctca 771
|||||

Sbjct: 361 ccaccacttcgctggcaactgttgactggatccaccagtgaccggacttctca 415

Score = 196 bits (99), Expect = 5e-47
Identities = 113/120 (94%)
Strand = Plus / Plus

Query: 179 tgttatTTTTcaagttatctttgtattgcagtcaaaagtagctagcgtaagaggaagat 238
|||||
Sbjct: 61 tgttatTTTTcaagttatctttgtattgcagtcaaaagtagctagcgtaagaggaagat 120

Query: 239 tttgcgaggttccccccacnnnnnnngttcttaaaaagaacaaaatgcatcctccagaaa 298
|||||
Sbjct: 121 tttgcgaggttccccccacttttttgttcttaaaaagaacaaaatgcatcctccagaaa 180

Score = 176 bits (89), Expect = 5e-41
Identities = 112/121 (92%), Gaps = 2/121 (1%)
Strand = Plus / Plus

Query: 299 tttgcgaggttccccccacnnnnnnngttcttaaaaagaacaaaatgcatcctccagaaa 358
|||||
Sbjct: 121 tttgcgaggttccccccacttttttgttcttaaaaagaacaaaatgcatcctccagaaa 180

Query: 359 --accaccaagatggcttcagttcggttcatggtgacaccgacaaagatcgatgacattc 416
|||||
Sbjct: 181 ccaccaccaagatggcttcagttcggttcatggtgacaccgacaaagatcgatgacattc 240

Query: 417 c 417
|
Sbjct: 241 c 241

Score = 145 bits (73), Expect = 2e-31
Identities = 73/73 (100%)
Strand = Plus / Plus

Query: 779 accacttcgctggcaactgttgactggatccaccagtgaccggacttctcaccgccag 838
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Sbjct: 363 accacttcgctggcaactgttgactggatccaccagtgaccggacttctcaccgccag 422

Query: 839 gatgtcatcgagg 851
|||||
Sbjct: 423 gatgtcatcgagg 435

Score = 119 bits (60), Expect = 9e-24
Identities = 60/60 (100%)
Strand = Plus / Plus

*results of* **BLAST****BLASTN 2.2.6 [Apr-09-2003]**Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1070309502-22860-148700428989.BLASTQ3

Query=

(4260 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

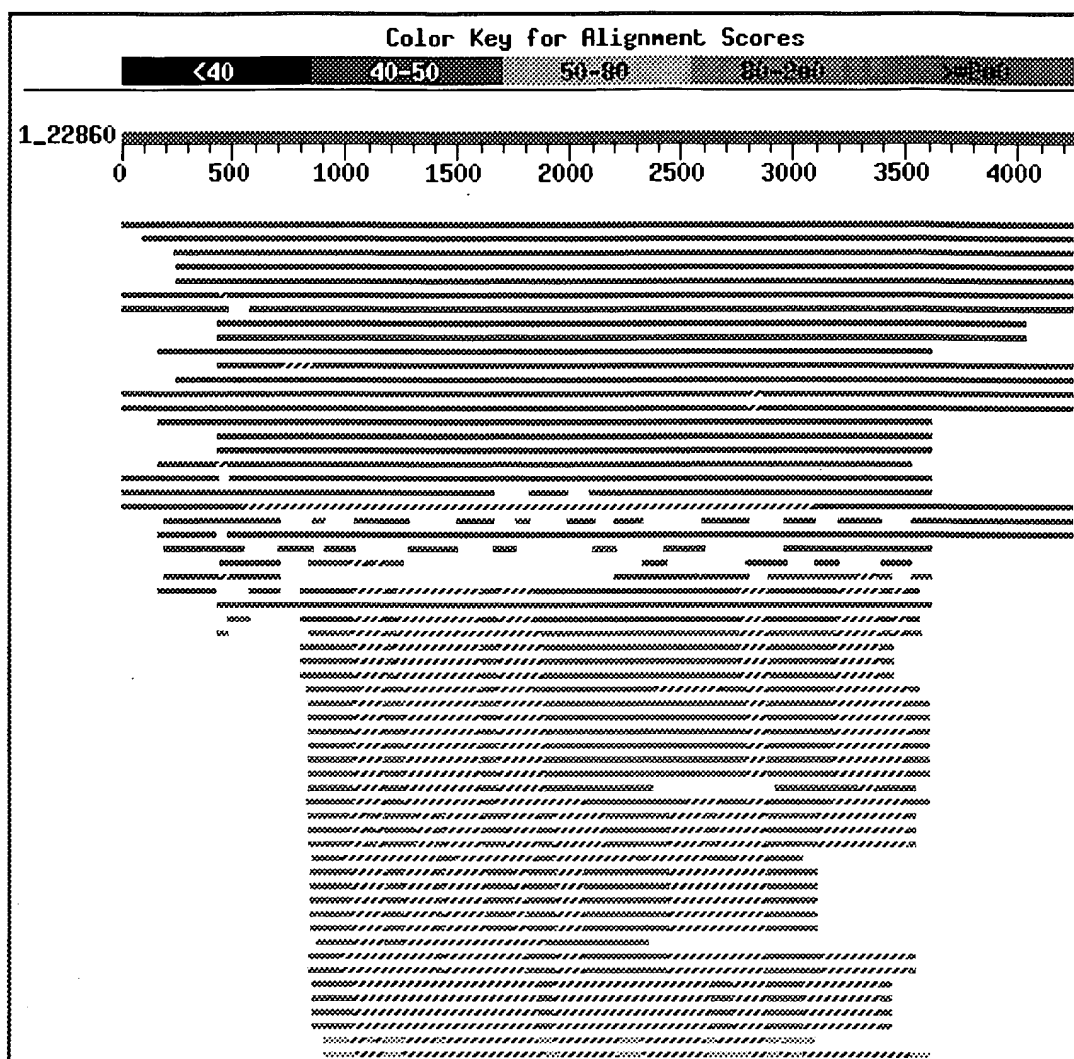
1,981,639 sequences; 9,522,297,199 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 358 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

	Score	E	
	(bits)	Value	

gi 5106522 gb AF105366.1 AF105366	Homo sapiens K-CI cotrans...	8227	0.0	
gi 21707904 gb BC033894.1 	Homo sapiens, solute carrier fam...	8027	0.0	
gi 33329255 gb AF531260.1 	Homo sapiens K-CI cotransporter ...	7791	0.0	
gi 33329253 gb AF531259.1 	Homo sapiens K-CI cotransporter ...	7787	0.0	
gi 19110890 gb AF477977.1 	Homo sapiens K-CI cotransporter ...	7771	0.0	
gi 33329251 gb AF531258.1 	Homo sapiens K-CI cotransporter ...	7325	0.0	
gi 5912005 emb AL117500.1 HSM801017	Homo sapiens mRNA; cDNA...	7138	0.0	
gi 4826779 ref NM_005135.1 	Homo sapiens solute carrier fam...	7018	0.0	
gi 4585228 gb AF108831.1 AF108831	Homo sapiens K:CI cotrans...	7018	0.0	
gi 6693797 gb AF116242.1 AF116242	Homo sapiens K-CI cotrans...	6762	0.0	
gi 34535353 dbj AK128133.1 	Homo sapiens cDNA FLJ46254 fis,...	6629	0.0	
gi 30704365 gb BC051744.1 	Homo sapiens cDNA clone IMAGE:48...	5562	0.0	
gi 30704980 gb BC051709.1 	Homo sapiens mRNA similar to sol...	5426	0.0	
gi 34367354 emb BX648195.1 HSM808343	Homo sapiens mRNA; cDN...	5426	0.0	
gi 15042076 gb AF211854.1 AF211854	Mus musculus K-CI cotran...	4238	0.0	

gi 19526768 ref NM_133648.1 	Mus musculus solute carrier fa...	3933	0.0	
gi 15042078 gb AF211855.1 AF211855	Mus musculus K-Cl cotran...	3933	0.0	
gi 38565927 gb BC062099.1 	Mus musculus cDNA clone MGC:6965...	3782	0.0	
gi 34856647 ref XM_342489.1 	Rattus norvegicus similar to K...	2335	0.0	
gi 23959139 gb BC036323.1 	Mus musculus solute carrier fami...	1893	0.0	
gi 15208176 dbj AB070168.1 	Macaca fascicularis testis cDNA...	1855	0.0	
gi 22416426 gb AF314956.1 F314931S26	Homo sapiens potassium...	1368	0.0	
gi 24414566 gb AC079203.9 	Homo sapiens chromosome 15, clon...	1354	0.0	
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gi 26343082 dbj AK052910.1 	Mus musculus 16 days neonate he...	92	1e-14	
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gi 29336195 gb AC040162.5 	Homo sapiens chromosome 16 clone...	78	2e-10	
gi 20861690 ref XM_149244.1 	Mus musculus hypothetical gene...	78	2e-10	

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|5106522|gb|AF105366.1|AF105366](#) Homo sapiens K-Cl cotransporter KCC3a m
complete cds
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Score = 8227 bits (4150), Expect = 0.0
Identities = 4210/4237 (99%), Gaps = 2/4237 (0%)
Strand = Plus / Plus

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

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